AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A compound comprising two or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

   a)   the antigen binding regions consist of a single polypeptide chain;

   b)   the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; ~~and wherein~~

   c)   the compound has a bivalent or a multivalent structure; and wherein

   d)   the compound is glycosylated.

2. (Previously Presented) A compound as claimed in claim 1, wherein the compound further comprises covalently bonded carbohydrates.

3. (Previously Presented) A compound as claimed in claim 1, wherein at least one antigen binding region comprises a variable domain of a heavy antibody chain and a variable domain of a light antibody chain (sFv fragment).

4. (Original) A compound as claimed in claim 1, wherein the antigen binding region binds to a tumor-associated antigen (TAA).

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5. (Previously Presented) A compound as claimed in claim 4, wherein the TAA is selected from the group consisting of an N-CAM, PEM, EGF-R, Sialyl-Le^a, Sialyl-Le^X, TFβ, GICA, GD$_3$, GD$_2$, TAG72, CA125, the 24-25 kDa glycoprotein defined by Mab L6, and CEA.

6. (Previously Presented) A compound as claimed in claim 1, wherein the enzyme is selected from the group consisting of a lactamase, pyroglutamate aminopeptidase, D-aminopeptidase, oxidase, peroxidase, phosphatase, hydroxynitrile lyase, protease, esterase, carboxypeptidase and glycosidase.

7. (Previously Presented) A compound as claimed in claim 6, wherein the enzyme is a β-glucuronidase, which is selected from the group consisting of an *E. coli* β-glucuronidase, a *Kobayasia nipponica* β-glucuronidase, a *Secale cereale* β-glucuronidase and a human β-glucuronidase.

8. (Original) A compound as claimed in claim 1, wherein the antigen binding region is linked to the enzyme via a peptide linker.

9. (Previously Presented) A compound as claimed in claim 2, wherein glycosylation covalently bonds the carbohydrates to the compound, and the glycosylation takes place either by means of chemical methods or by a selection of suitable expression systems.

10. (Previously Presented) A compound as claimed in claim 1, which has undergone secretory expression in *Saccharomyces cerevisiae* or in *Hansenula polymorpha*.

11. (Previously Presented) A compound as claimed in claim 1, which is expressed in *E. coli* and is subsequently chemically glycosylated.

12. (Currently Amended) A compound as claimed in claim 30, wherein the sFv-β-lactamase fusion protein has undergone periplasmic expression in *E. coli* and is <u>subsequently</u> chemically glycosylated.

13. (Previously Presented) A compound as claimed in claim 30, wherein the sFv-β-lactamase fusion protein has undergone secretory expression in *Saccharomyces cerevisiae* or *Hansenula polymorpha*.

14. (Withdrawn) A nucleic acid coding for a compound as claimed in claim 1.

15. (Withdrawn) A nucleic acid as claimed in claim 14, coding for a humanized sFv fragment against CEA and a human β-glucuronidase.

16. (Withdrawn) A nucleic acid as claimed in claim 14 with the sequence

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CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA          50

ATCTACATGG TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA          100

GATCACAGTT CTCTCTACAG TTACTGAGCA CACAGGACCT CACC ATG GGA TGG    153
                                                Met Gly     Trp
AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGTAAGGGGC      199
Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
                                             -10
TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG ACAATAGACAT         249

CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA CTG CAG    298
                          Gly Val His Ser Gln Val Gln Leu Gln
                                                1
GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG     343
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu
                     10
ACC TGC ACC GTG TCT GGC TTC ACC ATC AGC AGT GGT TAT AGC TGG     388
Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly Tyr Ser Trp
                                             30
CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA     433
His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly
                 40


TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC CCC TCT CTC AAA     478
Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys
                                 60
AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC CAG TTC AGC     523
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                    Ser  Arg  Val  Thr  Met  Leu  Val  Asp  Thr  Ser  Lys  Asn  Gln  Phe  Ser
                                    70                                       80
CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC TAT TAT          568
Leu  Arg  Leu  Ser  Ser  Val  Thr  Ala  Ala  Asp  Thr  Ala  Val  Tyr  Tyr
                                              90
TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC TGG          613
Cys  Ala  Arg  Glu  Asp  Tyr  Asp  Tyr  His  Trp  Tyr  Phe  Asp  Val  Trp
                    100                                       110
GGC CAA CCC ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG          658
Gly  Gln  Gly  Thr  Thr  Val  Thr  Val  Ser  Ser  Gly  Gly  Gly  Gly  Ser
                                                        120
GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC          703
Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Asp  Ile  Gln  Leu  Thr
                    130                                       140
CAG AGC CCA AGC AGC CTG AGC GCC AGC CTC GGT GAC AGA GTG ACC          748
Gln  Ser  Pro  Ser  Ser  Leu  Ser  Ala  Ser  Val  Gly  Asp  Arg  Val  Thr
                                              150
ATC ACC TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC          793
Ile   Thr  Cys  Ser  Thr  Ser  Ser  Ser  Val  Ser  Tyr  Met  His  Trp  Tyr
                              160                                   170
CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA          838
Gln  Gln  Lys  Pro  Gly  Lys  Ala  Pro  Lys  Leu  Leu  Ile  Tyr  Ser  Thr
                                              180
TCC AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT          883
Ser  Asn  Leu  Ala  Ser  Gly  Val  Pro  Ser  Arg  Phe  Ser  Gly  Ser  Gly
                    190                                       200
AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG          928
Ser  Gly  Thr  Asp  Phe  Thr  Phe  Thr  Ile  Ser  Ser  Leu  Gln  Pro  Glu
                                              210
GAC ATC GCC ACC TAC TAC TGC CAT CAG TGG AGT AGT TAT CCC ACG          973
Asp  Ile  Ala  Thr  Tyr  Tyr  Cys  His  Gln  Trp  Ser  Ser  Tyr  Pro  Thr
                    220                                       230
TTC GGC CAA GGG ACC AAG CTG GAG ATC AAA GGTGAGTAGA ATTTAAACTTT  1023
Phe  Gly  Gln  Gly  Thr  Lys  Leu  Glu  Ile  Lys
                                    240
TGCTTCCTCA GTTGGATCTG AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA 1077
                                                        Glu  Leu  Lys


ACC CCA CTT GGT GAC ACA ACT CAC ACA TGC CCA CGG TGC CCA          1119
Thr  Pro  Leu Gly  Asp  Thr  Thr  His  Thr  Cys  Pro  Arg  Cys  Pro
                              250
GGTAAGCCAG CCCAGGACTC GCCCTCCAGC TCAAGGCGGG ACAAGAGCCC          1169

TAGAGTGGCC TGAGTCCAGG GACAGGCCC AGCAGGGTGC TGACGCATCC           1219
ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG GCG GCG    1271
                                                        Ala  Ala  Ala
                                                             260
GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG CGG      1316
Ala  Val  Gln  Gly  Gly  Met  Leu  Tyr  Pro  Gln  Glu  Ser  Pro  Ser  Arg
                                              270
GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC      1361
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      Glu   Cys  Lys  Glu   Leu  Asp  Gly  Leu  Trp  Ser  Phe  Arg  Ala  Asp  Phe
                  280                                           290
      TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG              1406
      Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg
                                    300
      CCG CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC              1451
      Pro  Leu  Trp  Glu  Ser  Gly  Pro  Thr  Val  Asp  Met  Pro  Val  Pro  Ser
                  310                                           320
      AGC TTC AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC              1496
      Ser  Phe Asn Asp  Ile  Ser  Gln Asp  Trp  Arg  Leu  Arg  His  Phe  Val
                                    330
      GGC TGG GTG TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG              1541
      Gly  Trp  Val  Trp  Tyr Glu  Arg  Glu  Val  Ile  Leu Pro  Glu  Arg  Trp
                  340                                           350
      ACC CAG GAC CTG CGC ACA AGA GTG GTG CTG AGG ATT GGC AGT GCC              1586
      Thr  Gln  Asp Leu  Arg  Thr  Arg  Val  Val  Leu  Arg  Ile  Gly  Ser  Ala
                                    360
      CAT TCC TAT GCC ATC GTG TGG GTG AAT GGG GTC GAC ACG CTA GAG              1631
      His  Ser  Tyr  Ala  Ile  Val  Trp  Val Asn Gly  Val  Asp  Thr  Leu Glu
                  370                                           380
      CAT GAG GGG GGC TAC CTC CCC TTC GAG GCC GAC ATC AGC AAC CTG              1676
      His  Glu  Gly  Gly  Tyr  Leu  Pro  Phe Glu  Ala  Asp  Ile  Ser Asn Leu
                                    390
      GTC CAG GTG GGG CCC CTG CCC TCC CGG CTC CGA ATC ACT ATC GCC              1721
      Val  Gln  Val  Gly  Pro  Leu  Pro Ser  Arg  Leu Arg Ile  Thr  Ile  Ala
                  400                                           410
      ATC AAC AAC ACA CTC ACC CCC ACC ACC CTG CCA CCA GGG ACC ATC              1766
      Ile  Asn Asn  Thr  Leu Thr  Pro  Thr  Thr  Leu  Pro Pro  Gly  Thr  Ile
                                    420
      CAA TAC CTG ACT GAC ACC TCC AAG TAT CCC AAG GGT TAC TTT GTC              1811
      Gln  Tyr  Leu  Thr  Asp Thr  Ser  Lys  Tyr  Pro  Lys  Gly  Tyr  Phe Val
                  430                                           440
      CAG AAC ACA TAT TTT GAC TTT TTC AAC TAC GCT GGA CTG CAG CGG              1856
      Gln  Asn  Thr  Tyr  Phe  Asp  Phe Phe Asn  Tyr  Ala  Gly  Leu  Gln  Arg
                                    450
      TCT GTA CTT CTG TAC ACG ACA CCC ACC ACC TAC ATC GAT GAC ATC              1901
      Ser  Val  Leu  Leu  Tyr  Thr  Thr  Pro  Thr  Thr  Tyr  Ile  Asp  Asp Ile
                  460                                           470
      ACC GTC ACC ACC AGC GTG GAG CAA GAC AGT GGG CTG GTG AAT TAC              1946
      Thr  Val  Thr  Thr  Ser  Val  Glu  Gln  Asp  Ser  Gly  Leu  Val Asn Tyr
                                    480
      CAG ATC TCT GTC AAG GGC AGT AAC CTG TTC AAG TTG GAA GTG CGT              1991
      Gln  Ile  Ser  Val  Lys  Gly  Ser Asn  Leu  Phe  Lys  Leu Glu  Val  Arg
                  490                                           500
      CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG ACC              2036
      Leu  Leu  Asp  Ala  Glu  Asn  Lys  Val  Val  Ala  Asn Gly  Thr  Gly  Thr
                                    510
      CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC              2081
      Gln  Gly  Gln  Leu  Lys  Val  Pro  Gly  Val  Ser  Leu  Trp  Trp  Pro  Tyr
                  520                                           530
      CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG              2126
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       Leu  Met  His  Glu  Arg  Pro  Ala  Tyr  Leu  Tyr  Ser  Leu  Glu  Val  Gln
                                        540

       CTG  ACT  GCA  CAG  ACG  TCA  CTG  GGG  CCT  GTG  TCT  GAC  TTC  TAC  ACA        2171
       Leu  Thr  Ala  Gln  Thr  Ser  Leu  Gly  Pro  Val  Ser  Asp  Phe  Tyr  Thr
                              550                                          560

       CTC  CCT  GTG  GGG  ATC  CGC  ACT  GTG  GCT  GTC  ACC  AAG  AGC  CAG  TTC        2216
       Leu  Pro  Val  Gly  Ile  Arg  Thr  Val  Ala  Val  Thr  Lys  Ser  Gln  Phe
                                        570

       CTC  ATC  AAT  GGG  AAA  CCT  TTC  TAT  TTC  CAC  GGT  GTC  AAC  AAG  CAT        2261
       Leu  Ile  Asn  Gly  Lys  Pro  Phe  Tyr  Phe  His  Gly  Val  Asn  Lys  His
                              580                                          590

       GAG  GAT  GCG  GAC  ATC  CGA  GGG  AAG  GGC  TTC  GAC  TGG  CCG  CTG  CTG        2306
       Glu  Asp  Ala  Asp  Ile  Arg  Gly  Lys  Gly  Phe  Asp  Trp  Pro  Leu  Leu
                                        600

       GTG  AAG  GAC  TTC  AAC  CTG  CTT  CGC  TGG  CTT  GGT  GCC  AAC  GCT  TTC        2351
       Val  Lys  Asp  Phe  Asn  Leu  Leu  Arg  Trp  Leu  Gly  Ala  Asn  Ala  Phe
                              610                                          620

       CGT  ACC  AGC  CAC  TAC  CCC  TAT  GCA  GAG  GAA  GTG  ATG  CAG  ATG  TGT        2396
       Arg  Thr  Ser  His  Tyr  Pro  Tyr  Ala  Glu  Glu  Val  Met  Gln  Met  Cys
                                        630

       GAC  CGC  TAT  GGG  ATT  GTG  GTC  ATC  GAT  GAG  TGT  CCC  GGC  GTG  GGC        2441
       Asp  Arg  Tyr  Gly  Ile  Val  Val  Ile  Asp  Glu  Cys  Pro  Gly  Val  Gly
                              640                                          650

       CTG  GCG  CTG  CCG  CAG  TTC  TTC  AAC  AAC  GTT  TCT  CTG  CAT  CAC  CAC        2486
       Leu  Ala  Leu  Pro  Gln  Phe  Phe  Asn  Asn  Val  Ser  Leu  His  His  His
                                        660

       ATG  CAG  GTG  ATG  GAA  GAA  GTG  GTG  CGT  AGG  GAC  AAG  AAC  CAC  CCC        2531
       Met  Gln  Val  Met  Glu  Glu  Val  Val  Arg  Arg  Asp  Lys  Asn  His  Pro
                              670                                          680

       GCG  GTC  GTG  ATG  TGG  TCT  GTG  GCC  AAC  GAG  CCT  GCG  TCC  CAC  CTA        2576
       Ala  Val  Val  Met  Trp  Ser  Val  Ala  Asn  Glu  Pro  Ala  Ser  His  Leu
                                        690

       GAA  TCT  GCT  GGC  TAC  TAC  TTG  AAG  ATG  GTG  ATC  GCT  CAC  ACC  AAA        2621
       Glu  Ser  Ala  Gly  Tyr  Tyr  Leu  Lys  Met  Val  Ile  Ala  His  Thr  Lys
                              700                                          710

       TCC  TTG  GAC  CCC  TCC  CGG  CCT  GTG  ACC  TTT  GTG  AGC  AAC  TCT  AAC        2666
       Ser  Leu  Asp  Pro  Ser  Arg  Pro  Val  Thr  Phe  Val  Ser  Asn  Ser  Asn
                                        720

       TAT  GCA  GCA  GAC  AAG  GGG  GCT  CCG  TAT  GTG  GAT  GTG  ATC  TGT  TTG        2711
       Tyr  Ala  Ala  Asp  Lys  Gly  Ala  Pro  Tyr  Val  Asp  Val  Ile  Cys  Leu
                              730                                          740

       AAC  AGC  TAC  TAC  TCT  TGG  TAT  CAC  GAC  TAC  GGG  CAC  CTG  GAG  TTG        2756
       Asn  Ser  Tyr  Tyr  Ser  Trp  Tyr  His  Asp  Tyr  Gly  His  Leu  Glu  Leu
                                        750

       ATT  CAG  CTG  CAG  CTG  GCC  ACC  CAG  TTT  GAG  AAC  TGG  TAT  AAG  AAG        2801
       Ile  Gln  Leu  Gln  Leu  Ala  Thr  Gln  Phe  Glu  Asn  Trp  Tyr  Lys  Lys
                              760                                          770

       TAT  CAG  AAG  CCC  ATT  ATT  CAG  AGC  GAG  TAT  GGA  GCA  GAA  ACG  ATT        2846
       Tyr  Gln  Lys  Pro  Ile  Ile  Gln  Ser  Glu  Tyr  Gly  Ala  Glu  Thr  Ile
                                        780

       GCA  GGG  TTT  CAC  CAG  GAT  CCA  CCT  CTG  ATG  TTC  ACT  GAA  GAG  TAC        2891
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Ala   Gly   Phe His   Gln   Asp Pro Pro   Leu Met   Phe Thr   Glu   Glu   Tyr
              790                                              800
CAG AAA AGT CTG CTA GAG CAG TAC CAT CTG GGT CTG GAT CAA AAA          2936
Gln   Lys Ser Leu   Leu Glu   Gln   Tyr   His   Leu Gly   Leu Asp Gln Lys
                                      810
CGC AGA AAA TAT GTG GTT GGA GAG CTC ATT TGG AAT TTT GCC GAT          2981
Arg   Arg   Lys Tyr   Val   Val   Gly   Glu   Leu Ile   Trp Asn   Phe Ala   Asp
              820                                              830
TTC ATG ACT GAA CAG TCA CCG ACG AGA GTG CTG GGG ATT AAA AAG          3026
Phe   Met   Thr   Glu   Gln   Ser   Pro   Thr   Arg   Val   Leu Gly   Asn Lys   Lys
                                      840
GGG ATC TTC ACT CGG CAG AGA CAA CCA AAA AGT GCA GCG TTC CTT          3071
Gly   Ile   Phe Thr   Arg   Gln   Arg   Gln   Pro   Lys Ser   Ala   Ala   Phe Leu
              850                                              860
TTG CGA GAG AGA TAC TGG AAG ATT GCC AAT GAA ACC AGG TAT CCC          3116
Leu   Arg Glu Arg   Tyr   Trp   Lys   Ile   Ala   Asn Glu   Thr   Arg   Tyr   Pro
                                      870
CAC TCA GTA GCC AAG TCA CAA TGT TTG GAA AAC AGC CCG TTT ACT          3161
His   Ser Val   Ala   Lys Ser Gln   Cys   Leu Glu   Asn Ser   Pro   Phe Thr
              880                                              890
TGA GCAAGACTGA TACCACCTGC GTGTCCCTTC CTCCCCGAGT CAGGGCGACT 3214

TCCACAGCAG CAGACAAGT GCCTCCTGGA CTGTTCACGG CAGACCAGAA          3264

CGTTTCTGGC CTGGGTTTTG TGGTCATCTA TTCTAGCAGG GAACACTAAA          3314.
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17. (Withdrawn) A vector containing a nucleic acid as claimed in claim 14.

18. (Withdrawn) A host cell containing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17.

19. (Withdrawn) A host cell as claimed in claim 18, which is a BHK, CHO, COS, HeLa, insect, tobacco plant, yeast or *E. coli* cell.

20. (Withdrawn) A transgenic mammal with the exception of a human, containing a DNA as claimed in claim 14 or a vector as claimed in claim 17.

21. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises

    a) introducing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17 into a host cell,

    b) cultivating the host cell, and

c) isolating the compound.

22. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises

    a) cultivating a host cell as claimed in claim 18, and

    b) isolating the compound.

23. (Canceled).

24. (Canceled).

25. (Previously Presented) A pharmaceutical composition comprising a compound as claimed in claim 1 and a physiologically acceptable carrier.

26. (Previously Presented) A diagnostic aid comprising a compound as claimed in claim 1.

27. (Previously Presented) A compound as claimed in claim 6, wherein the lactamase enzyme is a *Bacillys cereus β*-lactamase II.

28. (Previously Presented) A compound as claimed in claim 6, wherein the carboxypeptidase enzyme is a carboxypeptidase G2 from *Pseudomonas*.

29. (Previously Presented) A compound as claimed in claim 10, which has undergone secretory expression in *Hansenula polymorpha*.

30. (Currently Amended) A compound as claimed in claim 1, wherein at ~~lease~~ least one antigen binding region and at least one prodrug-activating enzyme form an sFv-*β*-lactamase fusion protein.

31. (Previously Presented) A compound as claimed in claim 11, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

32. (Previously Presented) A compound as claimed in claim 12, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

33. (Previously Presented) A method of treating cancer comprising administering a compound claimed in claim 1 to a host in need thereof and subsequently administering a prodrug to be activated by the enzyme portion of the compound of claim 1.

34. (Currently Amended) A compound comprising one or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

a)   the antigen binding regions consist of a single polypeptide chain;

b)   the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; and wherein

c)   the compound has a monovalent, bivalent, or multivalent structure; and wherein

d)   the compound is glycosylated.

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